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OM protein - protein search, using sw model

Run on: Jun 25, 2003, 14:20:45 ; Search time 5.76512 Seconds
(without alignments)
798.574 Million cell updates/sec

Title: US-09-622-613b-26
Perfect score: 606
Sequence: 1 MSNMAFPQOKHINFTIILN.....ICVCEQYVHAGIGRCP 111

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 6
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	586.5	96.8	111	1	RNPO_RANCA
2	450	74.3	111	1	LECSLRNJA
3	369	60.9	111	1	RNPL_RANCA
4	272.5	45.0	104	1	RN30_RANPI
5	154.5	25.5	145	1	ANG3_MOUSE
6	149.5	24.7	145	1	ANGR_MOUSE
7	135.5	22.4	124	1	RNP_BALAC
8	135.5	22.4	145	1	ANGI_MOUSE
9	133.5	22.0	167	1	RNBR_BOVIN
10	132.5	21.9	124	1	RNP_PIG
11	128.5	21.2	151	1	RNBR_CAPCA
12	127.5	21.0	123	1	ANG2_BOVIN
13	127.5	21.0	141	1	RNBR_LIRCA
14	127.5	21.0	151	1	RNBR_LAXIPR
15	126.5	20.9	119	1	RNP_IGUIG
16	126.5	20.9	146	1	ANGI_CERAE
17	126.5	20.9	146	1	ANGI_MIOFA
18	125	20.6	146	1	ANGI_SATSC
19	123.5	20.4	143	1	RNBR_SHEEP
20	122.5	20.2	124	1	RNP_ANRAM
21	122	20.1	122	1	RNP_MACRU
22	120.5	19.9	128	1	RNP_MYOCO
23	120.5	19.9	147	1	ANGI_PONPY
24	120.5	19.9	149	1	RNP_MOUSE
25	120	19.8	146	1	ANGI_AOTTR
26	119.5	19.7	123	1	ANGI_PIG
27	118.5	19.6	128	1	RNBR_CAVPO
28	118	19.5	146	1	ANGI_SAGOE
29	117.5	19.4	128	1	RNP_HORSE
30	116.5	19.2	124	1	RNP_CANDU
31	116.5	19.2	128	1	RNP_PROGU
32	115.5	19.1	146	1	ANGI_MACMU
33	114	18.8	148	1	ANGI_BOVIN

ALIGNMENTS

RESULT 1	ID	RNPO_RANCA	STANDARD:	PRT:	111 AA.
AC	P11916:				
DF	01-OCT-1989 (Rel. 12, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (Stallid acid-binding lectin) (SBL-C).				
OS	Rana catesbeiana (Bull. frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.				
OX	NCBI_TaxID=8400;				
RP	SEQUENCE.				
RC	TISSUE=Egg;				
RX	MEDLINE=87299649; PubMed=3304421;				
FA	Tilani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawachi H., Takayanagi G., Hakomori S.;				
RT	"Amino acid sequence of stailic acid binding lectin from frog (Rana catesbeiana) eggs.";				
RL	Biochemistry 26:2189-2194(1987).				
RN	[2]				
RP	CHARACTERIZATION, AND SEQUENCE OF 59-79.				
RX	MEDLINE=92220613; PubMed=1373237;				
FA	Liao Y.-D.;				
RT	"A pyrimidine-guanine sequence-specific ribonuclease from Rana catesbeiana (bullfrog) oocytes.";				
RL	Nucleic Acids Res. 20:1371-1377(1992).				
RN	[3]				
RP	CHARACTERIZATION.				
RC	TISSUE=Egg;				
RX	MEDLINE=93192604; PubMed=8448385;				
FA	Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawachi H., Takayanagi G., Hakomori S., Tilani K.;				
RT	"Ribonuclease activity of stailic acid-binding lectin from Rana catesbeiana eggs.";				
RL	Glycobiology 3:37-45(1993).				
RN	[4]				
RP	STRUCTURE BY NMR.				
RX	MEDLINE=98437383; PubMed=9761686;				
FA	Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;				
RT	"The solution structure of a cytotoxic ribonuclease from the oocytes of Rana catesbeiana (bullfrog).";				
RL	J. Mol. Biol. 283:231-244(1998).				
CC	-1- FUNCTION: PREFERENTIALLY CLEAVES SINGLE-STRANDED RNA AT PYRIMIDINE RESIDUES WITH A 3'-FLANKING GUANINE. HYDROLYSES POLY(U) AND POLY(C) AS SUBSTRATES, AND PREFERENCES THE FORMER. THE S-LLECTINS IN FROG EGGS MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG EMBryo. THIS LECTIN AGGLUTINATES VARIOUS ANIMAL CELLS, INCLUDING NORMAL LYMPHOCYTES, ERYTHROCYTES, AND FIBROBLASTS OF ANIMAL AND HUMAN ORIGIN.				
CC	-1- SUBUNIT: MONOMER.				
CC	-1- SUBCELLULAR LOCATION: Secreted.				
CC	-1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.				
DR	PIR; A27121; A27121.				

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DR PDB; 1BC4; 28-OCT-98 .  
DR InterPro: IPR001427; RNaseA.  
DR Pfam; PF00074; rnaase; 1.  
DR ProDom; PD000535; RNaseA; 1.  
DR SMART; SM00092; RNase_Pc; 1.  
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.  
KW Hydrolase; Nuclease; Endonuclease; Sialic acid; Lactin; 3D-structure.  
FT MOD_RES 1  
FT ACT_SITE 1  
FT ACT_SITE 10  
FT ACT_SITE 35  
FT ACT_SITE 103  
FT DISULFID 19  
FT DISULFID 34  
FT DISULFID 52  
FT DISULFID 93  
SO SEQUENCE 111 AA; 12464 MW; DBC9E5F55729ECFA CRC64;  
  
Query Match 96.8%; Score 586.5; DB 1; Length 111;  
Best Local Similarity 99.1%; Pred. No. 1.2e-56;  
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
  
OY 3 NMATFGQKHIIINTPLI-CNTIMDNNIYVGGQCKRVNFIISATTVKAICTGVINMVL 61  
Db 2 NMATFGQKHIIINTPLINCNTIMDNNIYVGGQCKRVNFIISSATTVKAITGVINMVL 61  
OY 62 STTRPQLTCTRTSTTPRPPCYSSRTETNYTCVKENQYPVHAGIGRCP 111  
Db 62 STTRPQLTCTRTSTTPRPPCYSSRTETNYTCVKENQYPVHAFGIGRCP 111  
  
RESULT 2  
LECS_RANJA STANDARD; PRT; 111 AA.  
AC PI8839;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Sialic acid-binding lectin (EC 3.1.27.-).  
OS Rana japonica (Japanese reedfish frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
OX NCBI_Taxid=8402;  
RN [1]  
RP SEQUENCE, AND DISULFIDE BONDS.  
RC TISSUE=Egg;  
RX MEDLINE=91035319; PubMed=2229005;  
RA Kamuya Y., Oyama F., Sakakibara F., Nitta K., Kawachi H.,  
RT Takeyanagi Y., Titani K.;  
RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.";  
RL J. Blochm. 108:139-143(1990).  
CC - FUNCTION: THE S-LECTINS IN PROG EGGS MAY BE INVOLVED IN THE  
CC FERTILIZATION AND DEVELOPMENT OF THE PROG EMBRYO. THIS LECTIN  
CC PREFERENTIALLY AGGLUTINATE A LARGE VARIETY OF TUMOR CELLS, BUT IT  
CC DOES NOT AGGLUTINATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.  
CC - SUBUNIT: MONOMER.  
CC - SUBCELLULAR LOCATION: Secreted.  
CC - SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
DR PIR: JX0120; JX0120.  
DR HSP: P11916; 1BC4.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam; PF00074; rnaase; 1.  
DR ProDom; PD000535; RNaseA; 1.  
DR SMART; SM00092; RNase_Pc; 1.  
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.  
KW Hydrolase; Nuclease; Endonuclease; Sialic acid; Lactin.  
FT MOD_RES 1  
FT ACT_SITE 1  
FT ACT_SITE 10  
FT ACT_SITE 35  
FT ACT_SITE 103  
FT DISULFID 19  
FT DISULFID 34  
FT DISULFID 52  
FT DISULFID 97
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FT	DISULFID	94	111	
5Q	SEQUENCE	111 AA:	12326 MW:	FDEBDDF3834ED679 CRC64:
	Query Match	74.3%:	Score 450:	DB 1: Length 111:
	Best Local Similarity	78.2%:	Pred. No. 6,6e-42:	
	Matches	86:	Conservative	7: Mismatches 15, Indels 2, Gaps 2
OY	3	NMAFPOOKHIIINTP	-IICNTIMDNNYIVYGOCRKRVNFIISATYVAICTGYI	-INNV 60
DB	2	NMAFEOEHKIHPTNSINICNTIMDNTSYIVYGOCRKERNFIISATYVAICTGASTNRV		61
OY	61	LSTRFQJLNTCTRTSTIRPCPYSSRRTETNYICVGCENQYPVHFAIGIRC		110
DB	62	LSTRFQJLNTCTRTSATAPRCPYNSTRRTNYICVGCENRLPVPVHFAIGIRC		111
	RESULT 3			
	RNPL_RANCA	STANDARD:	PRT:	111 AA.
ID	AC	PI4626:		
DT	01-APR-1990	(Rel. 14, Created)		
DT	01-FEB-1994	(Rel. 28, last sequence update)		
DT	15-JUN-2002	(Rel. 41, last annotation update)		
DE	Ribonuclease, liver (EC 3.1.27.5).			
OC	Rana catesbeiana (Bull frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.			
OX	NCHI_TaxID=8400;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Liver;			
RX	MEDLINE=90130374; PubMed=2613682;			
RA	Nitta R., Katayama N., Okabe Y., Iwana M., Watanabe H., Abe Y.,			
RT	Okazaki T., Ohgi K., Irie M.			
RT	"Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)			
RL	liver."			
RL	J. Biochem. 106:729-735(1989).			
CC	-I- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-			
CC	phosphates and 3'-phosphooligonucleotides ending in C-P or U-P			
CC	with 2',3'-cyclic phosphate intermediates.			
CC	-I- SUBCELLULAR LOCATION: Secreted.			
CC	-I- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.			
CC	PIR: JX0085; JX0085.			
DR	HSSP; F11916; IBC4.			
DR	InterPro: IPR001427; RNaseA.			
DR	Pfam: PF00074; RNaseA; 1.			
DR	ProDom: PD000535; RNaseA; 1.			
DR	SMART: SM00092; RNase_Pc; 1.			
DR	PROSITE: PS00127; RNASE_PANCREATIC; 1.			
KW	Hydrolase; Nuclease; Endonuclease.			
FT	MOD_RES	1		
FT	ACT_SITE	10		
FT	ACT_SITE	35		
FT	ACT_SITE	104		
FT	DISULFD	19		
FT	DISULFD	34		
FT	DISULFD	52		
FT	DISULFD	94		
SO	SEQUENCE	111 AA;	12461 MW;	D64BA72456C10788 CRC64:
	Query Match	60.9%:	Score 369:	DB 1: Length 111:
	Best Local Similarity	65.5%:	Pred. No. 3,7e-33:	
	Matches	72:	Conservative	9: Mismatches 27, Indels 2, Gaps 2
OY	3	NMAFPOOKHIIINTP	-CNTIMDNNYIVYGOCRKRVNFIISATYVAICTGYI	-NNNV 60
DB	2	NMAFKEKHIRSTSIDCNTIMDAIYIVGCKERNFTFIISSEDNVAICTGVSPPDKE		61
OY	61	LSTRFQJLNTCTRTSTIRPCPYSSRRTETNYICVGCENQYPVHFAIGIRC		110
DB	62	LSTRFQJLNTCTRTSTIRPCPYSSRRTETNYICVGCENQYPVHFAIGIRC		111

RESULT 4
 RN30_RANPI STANDARD: PRT: 104 AA.
 AC P22069:
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE P-30 protein (EC 3.1.27.-) (Onconase).
 OS Rana pipiens (Northern leopard frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
 NX NCBI_TaxID=8404;
 RX MEDLINE=9109311; PubMed=1985896;
 RC Tissue=Embryo;
 RA Ardelit W., Mikulski S.M., Shogen K.;
 RT "Amino acid sequence of an anti-tumor protein from Rana pipiens
 oocytes and early embryos. Homology to pancreatic ribonucleases."
 RL J. Biol. Chem. 266:245-251(1991).
 RN 3D-STRUCTURE MODELING:
 RX MEDLINE=9306156; PubMed=1438177;
 RA Mosmann S.C., Johns K.L., Ardelit W., Mikulski S.M., Shogen K.;
 RT "Comparative molecular modeling and crystallization of P-30 protein:
 a novel antitumor protein of Rana pipiens oocytes and early
 embryos."
 RL Proteins 14:392-400(1992).
 RN 3D-STRUCTURE MODELING:
 RX MEDLINE=9416079; PubMed=8120892;
 RA Mosmann S.C., Ardelit W., James M.N.G.;
 RT "Refined 1.7 Å x-ray crystallographic structure of P-30 protein, an
 amphibian ribonuclease with anti-tumor activity."
 RL J. Mol. Biol. 236:1141-1153(1994).
 CC -1- FUNCTION: BASIC PROTEIN WITH ANTI-PROLIFERATIVE/CYTOTOXIC ACTIVITY
 AGAINST SEVERAL TUMOR CELL LINES IN VITRO. AS WELL AS ANTITUMOR
 IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH
 MOLECULAR WEIGHT RIBOSOMAL RNA.
 CC -1- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PDB: 1ONC: 31-JAN-94.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 KW Hydrolyase; Nuclease; Endonuclease; 3D-structure.
 FT MOD_RES 1
 FT ACT_SITE 10
 FT ACT_SITE 31
 FT ACT_SITE 97
 FT DISULFID 19
 FT DISULFID 30
 FT DISULFID 48
 FT DISULFID 87
 FT HELIX 3
 FT STRAND 11
 FT STRAND 12
 FT HELIX 19
 FT TURN 22
 FT TURN 23
 FT TURN 24
 FT STRAND 33
 FT TURN 36
 FT HELIX 41
 FT TURN 49
 FT STRAND 50
 FT TURN 55
 FT STRAND 58
 FT TURN 63
 FT TURN 74
 FT TURN 75
 FT STRAND 77
 FT STRAND 84
 FT TURN 91
 FT TURN 93
 FT STRAND 101
 FT STRAND 101
 SEQUENCE 101 AA: 11845 MW: 22A753C2F9E566B4 CRC64:

Query Match 45.0%; Score 272.5; DB 1; Length 104;
 Best Local Similarity 49.1%; Pred. No. 9.2e-23;
 Matches 54; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
 Oy 3 MMATFOOKHIITN-PIICNTIMDNMIYIGGCKRVNFTIISATYKAICVTI-NMNV 60
 Db 2 DWLTFQKHIITNVDCCDINMSTNLF---HCKDKNTFYISRPDPYKAICKIISKV 57
 Oy 61 LSTRPOLNCTRTSITPRCPYSSRTETNYICKENQVPYFAGIGRC 110
 Db 58 LTTSEFLSDC---NVTSPCKYKLRKSTNKFVTCENQAPVHFVGVSC 104
 RESULT 5
 ANG3_MOUSE STANDARD: PRT: 145 AA.
 AC P97802;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Angiogenin-3 precursor (EC 3.1.27.-) (Angiogenin-related protein 2)
 DE (EF-5).
 GN ANG3 OR ANG1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=BAIB/C;
 RX MEDLINE=97184476; PubMed=9032278;
 RA Fu X., Kamps M.P.;
 RT "E2a-bx1 induces aberrant expression of tissue-specific and
 developmentally regulated genes when expressed in NIH 3T3
 fibroblasts."
 RL Mol. Cell. Biol. 17:1503-1512(1997).
 CC -1- FUNCTION: ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
 MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
 HYDROLYZING CELLULAR TRNAS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
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 between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 DR EMBL: U72672; AAC05794.1;
 DR HSSP: P10152; IAGI.
 DR MGD: MGI:1201793; Ang1.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
 KW Protein synthesis inhibitor; Signal.
 FT SIGNAL 1
 FT CHAIN 25
 FT MOD_RES 25
 FT ACT_SITE 37
 FT ACT_SITE 64
 FT ACT_SITE 137
 FT DISULFID 50
 FT DISULFID 63
 FT DISULFID 81
 FT DISULFID 130
 SEQUENCE 145 AA: 16696 MW: DE9D3BC92F1D682C CRC64:


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FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .)
FT CARBOHYD 155 155 /FTID-CAR_000005.
FT CARBOHYD 159 159 O-LINKED.
FT CONFLICT 155 155 O-LINKED.
SQ SEQUENCE 167 AA: 18450 MW: 681CAAC3CC2FC459 CRC64;

Query Match 22.0%; Score 133.5; DB 1; Length 167;
Best Local Similarity 31.4%; Pred. No. 1.5e-07;
Matches 38; Conservative 17; Mismatches 43; Indels 23; Gaps 7;

OY 5 ATPQKH-----INPIICNTIMDNNTIYVGGCKRVNTFIISATTVKATCTGYNM 58
D 32 AKFRROHMDGSSSSSNPNYCNOMMKRR-RMTGRCKPVTNFVHESLDYKAVCS---OK 87
OY 59 NVL-----STREFOLNTCTRTSTTPRP-CPYSSRTETNYICVKE-NOY-PVHFA 105
D 88 NITCKNGHPNCYQSKSTMSITDCRETGSSKTPNCAYKTSOKKITTVACBGNPVYPVHFD 147
OY 106 G 106
D 148 G 148

RESULT 10
RNP_PIG STANDARD; PRT; 124 AA.
AC P00671;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN RNASE1 OR RN51.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9623;
RN [1]
RP SEQUENCE.
RX MEDLINE=70104197; PubMed=5460946;
RA Jackson R.L., Hirs C.H.W.;
RT "The primary structure of porcine pancreatic ribonuclease. II. The
RT amino acid sequence of the reduced S-aminoethylated protein."
RL J. Biol. Chem. 245:637-653(1970).
RN [2]
RP REVISION TO 2.
RA Wieringa R.K., Huisinga J.D., Gaastra W., Wellington G.W., Beintema J.J.;
RT "Affinity chromatography of porcine pancreatic ribonuclease and
RT reinvestigation of the N-terminal amino acid sequence."
RL FEBS Lett. 31:181-185(1973).
RN [3]
RP DISULFIDE BONDS.
RX MEDLINE=70104198; PubMed=4904878;
RA Phelan J.J., Hirs C.H.W.;
RT "The primary structure of porcine pancreatic ribonuclease. 3. The
RT disulfide bonds."
RL J. Biol. Chem. 245:654-661(1970).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR HSSP: P00656; ISRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR PRODOM: PD000535; RNaseA.1.
DR SMART: SM00092; RNase_PC.1.
DR PROSITE: PS00127; RNASE_PANCREATIC.1.
KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84

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FT DISULFID 40 95
FT DISULFID 58 110
FT DISULFID 65 72
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .)
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .)
FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .)
SQ SEQUENCE 124 AA: 13804 MW: 0AC28CDE14111845 CRC64;

Query Match 21.9%; Score 132.5; DB 1; Length 124;
Best Local Similarity 31.6%; Pred. No. 1.5e-07;
Matches 36; Conservative 19; Mismatches 42; Indels 17; Gaps 6;

OY 7 FOQKH-----INPIICNTIMDNNTIYVGGCKRVNTFIISATTVKATCTGYNM 59
D 8 FÖRÖHMDPSSSSSNPNYCNLMMSRR-NMTÖGRCKPVTNFVHESLADQAVCSOINVCK 66
OY 60 VLASTREFOLNT-----CTRTSTTPRP-CPYSSRTETNYICVKE-NOY-PVHFA 104
D 67 NGÖTNCYQSNSTMTITCTGRTGSSKYPNCAYKASQEQKHIIIVACEGNPPVYPVH 120

RESULT 11
RNBR_CAPCA STANDARD; PRT; 151 AA.
AC P79351;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ribonuclease, brain (EC 3.1.27.-) (BRB).
OS Capreolus capreolus (Roe deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoides;
OC Cervidae; Odocoileinae; Capreolus.
OX NCBI_TaxID=9858;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98278842; PubMed=9611269;
RA Breukelman H.J., van der Munnik N., Kleinedam R.G., Furia A.,
RA Beintema J.J.;
RT "Secretory ribonuclease genes and pseudogenes in true ruminants."
RL Gene 212:259-268(1998).
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: Y11673; CAAT72371.1; .
DR HSSP: P00656; ISRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR PRODOM: PD000535; RNaseA.1.
DR SMART: SM00092; RNase_PC.1.
DR PROSITE: PS00127; RNASE_PANCREATIC.1.
KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
FT ACT_SITE 41 41 BY SIMILARITY.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT CARBOHYD 65 72 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT CARBOHYD 129 129 O-LINKED (BY SIMILARITY).
FT CARBOHYD 133 133 O-LINKED (BY SIMILARITY).
SQ SEQUENCE 151 AA: 16971 MW: 392DE65302F006A6 CRC64;

```

Query Match 21.2% Score 128.5; DB 1; Length 151;
 Best Local Similarity 29.4%; Pred. No. 4.8e-07;
 Matches 35; Conservative 17; Mismatches 44; Indels 23; Gaps 6;

OY 5 ATFOQKH-----INPIICNTIMDNNTIYVGQCKRVNFTIISATYKATCTGYIM 58
 D 6 AKFRCHMDSSSSSSGNCNMKRR-RMTHGRCKPVNTFVHESLDNVKAVCS---QK 61
 OY 59 NVL-----STRFQNTCTRTSTITPR-CPYSSRTETNTCYKCEMO--YPYHF 104
 D 62 NITCKNCPNCYOSNSTMNITDCRGTSKYPNCAYTSOKOKYITVACEGDPYVPHF 120

RESULT 12

ANG2_BOVIN STANDARD; PRT; 123 AA.
 AC P80929;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Angiogenin-2 (EC 3.1.27.-).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NC NCBI_TaxID=9913;
 RP [1]
 RE SEQUENCE.
 RC TISSUE=Serum, and Milk;
 RX MEDLINE=97409980; PubMed=9266695;
 RA Strydom D.J., Bond M.D., Vallee B.L.;
 RT "An angiogenic protein from bovine serum and milk -- purification and
 RL Eur. J. Biochem. 247:535-544(1997).
 CC -1- FUNCTION: BINDS TIGHTLY TO PLACENTAL RIBONUCLEASE INHIBITOR AND
 CC HAS VERY LOW RIBONUCLEASE ACTIVITY. HAS POTENT ANGIOGENIC
 CC ACTIVITY. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
 CC HYDROLYZING CELLULAR TRANS.
 CC -1- TISSUE SPECIFICITY: SERUM, AND MILK.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 CC DR HSSP: P10152; IAGI.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR PRODOM: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_PC; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 KM Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
 KW Protein synthesis inhibitor; Glycoprotein.
 FT MOD_RES 1 1
 FT ACT_SITE 12 12
 FT ACT_SITE 39 39 BY SIMILARITY.
 FT ACT_SITE 113 113 BY SIMILARITY.
 FT DISULFID 25 80 BY SIMILARITY.
 FT DISULFID 38 91
 FT CARBOHYD 56 106
 FT CARBOHYD 33 33
 SQ SEQUENCE 123 AA; 14522 MW; B703B9839919FD2F CRC64;

Query Match 21.0% Score 127.5; DB 1; Length 123;
 Best Local Similarity 30.6%; Pred. No. 5e-07;
 Matches 33; Conservative 19; Mismatches 43; Indels 13; Gaps 5;

OY 7 FQCKHIINTPI-----ICNTIMDNNTIYVGQCKRVNFTIISATYKATCTGYIM 58
 D 8 AKFRCHMDSSSSSSGNCNMKRR-RMTHGRCKPVNTFVHESLDNVKAVCS---QK 61
 OY 59 NVLSTTR--TQNTCTRTSTITPR-CPYSSRTETNTCYKCEMO--YPYHF 103
 D 66 NGLFSSSPFOVYTCRHRGSGPRPCRYRAFRANRIVIVRCRDGPFH 113

RESULT 13

RNBR_GIRCA STANDARD; PRT; 141 AA.
 AC Q29542; Q29533;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ribonuclease, brain (EC 3.1.27.-) (Brb).
 GN BRN.
 OS Giraffa camelopardalis (Giraffe).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Giraffidae;
 OC Giraffidae; Giraffa.
 NC NCBI_TaxID=98994;
 RP [1]
 RE SEQUENCE FROM N.A.
 RX MEDLINE=96139017; PubMed=8587129;
 RA Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
 RA Vento M.T., Furla A.;
 RT "Molecular evolution of genes encoding ribonucleases in ruminant
 RT species".
 RL J. Mol. Evol. 41:850-858(1995).
 CC [2]
 CC SEQUENCE OF 31-114 FROM N.A.
 RX MEDLINE=93367815; PubMed=8360916;
 RA Breukelman H.J., Beintema J.J., Confalone E., Costanzo C., Sasso M.P.,
 RA Carsana A., Palmieri M., Furla A.;
 RT "The genomic DNA of mammalian species".
 RL J. Mol. Evol. 37:29-35(1993).
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

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 CC -----
 CC DR EMBL: S81743; AAB36137.1; -;
 CC DR EMBL: S65126; AAB27931.1; -;
 CC DR HSSP: P00656; 2RNS.
 CC DR InterPro: IPR001427; RNaseA.
 CC DR Pfam: PF00074; RNaseA; 1.
 CC DR PRINTS: PR00794; RIBONUCLEASE.
 CC DR PRODOM: PD000535; RNaseA; 1.
 CC DR SMART: SM00092; RNase_PC; 1.
 CC DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 CC DR Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
 CC FT ACT_SITE 41 41
 CC FT ACT_SITE 26 84 BY SIMILARITY.
 CC FT DISULFID 40 95 BY SIMILARITY.
 CC FT DISULFID 58 110 BY SIMILARITY.
 CC FT DISULFID 65 72 BY SIMILARITY.
 CC FT CARBOHYD 62 62
 CC FT CARBOHYD 129 129
 CC FT CARBOHYD 129 129
 CC SQ SEQUENCE 141 AA; 15592 MW; 73745E9079591F CRC64;

Query Match 21.0% Score 127.5; DB 1; Length 141;
 Best Local Similarity 30.6%; Pred. No. 5.8e-07;
 Matches 37; Conservative 17; Mismatches 44; Indels 23; Gaps 7;

OY 5 ATFOQKH-----INPIICNTIMDNNTIYVGQCKRVNFTIISATYKATCTGYIM 58
 D 6 AKFRCHMDSSSSSSGNCNMKRR-RMTHGRCKPVNTFVHESLDNVKAVCS---QK 61
 OY 59 NVL-----STRFQNTCTRTSTITPR-CPYSSRTETNTCYKCE--NYY-PVHFA 105
 D 62 NITCKNCPNCYOSNSTMNITDCRGTSKYPNCAYTSOKOKYITVACEGDPYVPHF 121
 OY 106 G 106

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Db      122 G 122

RESULT 14
RNRB_AXIPR STANDARD: PRT: 151 AA.
ID RNRB_AXIPR
AC P87350;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ribonuclease, brain (EC 3.1.27.-) (BRB).
CN BRN.
OS Axis porcinus (Hog deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Cervinae; Axis.
OX NCBI_TaxID=57737;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98278842; Pubmed=9611269;
RA Breukelman H.J., van der Munik N., Kleinedam R.G., Furia A.,
RA Beintema J.J.;
RT "Secretory ribonuclease genes and pseudogenes in true ruminants.";
RL Gene 212:259-268(1998).
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY
CC -----
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CC -----
DR EMBL: Y11670; CAA72368.1;
DR HSSP: P00656; 1SRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR ProDom: PD000535; RNaseA.1.
DR SMART: SM00092; RNaseA.Pc.1.
DR PROSITE: PS00127; RNase_PANCREATIC.1.
KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
FT ACT_SITE 41 41
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT CARBOHYD 65 72 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC...) (BY SIMILARITY).
FT CARBOHYD 129 129 O-LINKED (BY SIMILARITY).
FT CARBOHYD 133 133 O-LINKED (BY SIMILARITY).
SQ SEQUENCE 151 AA; 16819 MW; E95F3757FEC5E233 CRC64;

Query Match 21.0%; Score 127.5; DB 1; Length 151;
Best Local Similarity 30.6%; Pred. No. 6.2e-07;
Matches 37; Conservative 17; Mismatches 44; Indels 23; Gaps 7;

OY 5 ATFOOKHI-----INPILCNTIMDNIIYIGGCKRNVNFIISATVKAICTGVINM 58
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 6 AKFRQHHDAGSSSSGNSNYSNOMKRR-RMTHGCKPNTFVHESLDSYKAVCS---QK 61
OY 59 NVL-----STTRFQNLNCTRTSTITPRP-CPYSSRTETNYICVCE-NQY-PVHFA 105
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 62 NITCKNGOPNCYOSNSTWNTINDCKRETGSSKIPNCAYKTSOKOKIITVACGPNVPHFD 121
OY 106 G 106
Db 122 G 122

RESULT 15
RNP_IGUG
RNP_IGUG

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ID RNP_IGUG STANDARD: PRT: 119 AA.
AC P80287;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
OS Iguana iguana (Common Iguana).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
OX NCBI_TaxID=6517;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=94139745; Pubmed=8307028;
RA Zhao W., Beintema J.J., Hofsteenge J.;
RT "The amino acid sequence of iguana (Iguana iguana) pancreatic
RT ribonuclease.";
RL Eur. J. Biochem. 219:641-646(1994).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR HSSP: P00656; 1LSQ.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR ProDom: PD000535; RNaseA.1.
DR SMART: SM00092; RNaseA.Pc.1.
DR PROSITE: PS00127; RNase_PANCREATIC.1.
KW Hydrolyase; Nuclease; Endonuclease.
FT MOD_RES 1 1 PYROGLUTAMINE CARBOXYLIC ACID.
FT DISULFID 25 80 BY SIMILARITY.
FT DISULFID 39 91 BY SIMILARITY.
FT DISULFID 57 106 BY SIMILARITY.
FT ACT_SITE 10 10 BY SIMILARITY.
FT ACT_SITE 40 40 BY SIMILARITY.
FT ACT_SITE 113 113 BY SIMILARITY.
SQ SEQUENCE 119 AA; 13324 MW; 6072FB5B7B15BD5A CRC64;

Query Match 20.9%; Score 126.5; DB 1; Length 119;
Best Local Similarity 29.8%; Pred. No. 6.2e-07;
Matches 34; Conservative 16; Mismatches 51; Indels 13; Gaps 4;

OY 3 NMATFOOKHI-----INPILCNTIMDNIIYIGGCKRNVNFIISATVKAICTGVINM 52
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 2 DMSRQNHNDIYPTETASNPNAVCYCDLMMQRR-NLNPTRCKTRNTFVHASPSEIQVCGSG 60
OY 53 -TGVINNVNLTTRFQNLNCTRTSTIT-PRCPYSSRTETNYICVCE-NQY-PVHFA 104
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 61 GTHYEDNLNDYNSFSLTDCKNVGGTAVSSCKYNQTPQTRKIRLACENNQYVHF 114

Search completed: June 25, 2003, 14:50:07
Job time : 5.76512 secs

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